



Revised Sequence Listing filed 2006-07-26
SEQUENCE LISTING

<110> KATO, Seishi
NAGATA, Naoki
FUJIMURA, Naoko
KOBAYASHI, Midori
ITO, Koichi
ISHIZUKA, Yoshiko

<120> A Method For Producing An Antibody By Gene Immunization

<130> 2002_0400A

<140> 10/088,859

<141> 2002-05-29

<150> PCT/JP01/06371

<151> 2001-07-24

<150> PCT2000-222743

<151> 2000-07-24

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<151> 2000-08-24

<160> 18

<170> PatentIn version 3.3

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1 5

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10 15 20

gtt aaa cta act cga gat tct cag agt tta tgc ccc tat gat tgg att 270
Val Lys Leu Thr Arg Asp Ser Gln Ser Leu Cys Pro Tyr Asp Trp Ile
25 30 35 40

ggt ttc caa aac aaa tgc tat tat ttc tct aaa gaa gaa gga gat tgg 318
Gly Phe Gln Asn Lys Cys Tyr Tyr Phe Ser Lys Glu Glu Gly Asp Trp
45 50 55

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Asn Ser Ser Lys Tyr Asn Cys Ser Thr Gln His Ala Asp Leu Thr Ile
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Ile Asp Asn Ile Glu Glu Met Asn Phe Leu Arg Arg Tyr Lys Cys Ser	
75 80 85	
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Ser Asp His Trp Ile Gly Leu Lys Met Ala Lys Asn Arg Thr Gly Gln	
90 95 100	
tgg gta gat gga gct aca ttt acc aaa tcg ttt ggc atg aga ggg agt	510
Trp Val Asp Gly Ala Thr Phe Thr Lys Ser Phe Gly Met Arg Gly Ser	
105 110 115 120	
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Glu Gly Cys Ala Tyr Leu Ser Asp Asp Gly Ala Ala Thr Ala Arg Cys	
125 130 135	
tac acc gaa aga aaa tgg att tgc agg aaa aga ata cac taa	600
Tyr Thr Glu Arg Lys Trp Ile Cys Arg Lys Arg Ile His	
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Ser Leu Cys Pro Tyr Asp Trp Ile Gly Phe Gln Asn Lys Cys Tyr Tyr
35 40 45
Phe Ser Lys Glu Glu Gly Asp Trp Asn Ser Ser Lys Tyr Asn Cys Ser
50 55 60
Thr Gln His Ala Asp Leu Thr Ile Ile Asp Asn Ile Glu Glu Met Asn
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Phe Leu Arg Arg Tyr Lys Cys Ser Ser Asp His Trp Ile Gly Leu Lys
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Met Ala Lys Asn Arg Thr Gly Gln Trp Val Asp Gly Ala Thr Phe Thr
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Lys Ser Phe Gly Met Arg Gly Ser Glu Gly Cys Ala Tyr Leu Ser Asp
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Ala Val Glu Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile
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Ser Asp Val Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp
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Lys Val Tyr Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile
45 50 55

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75 80 85

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Ile Tyr Val Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala
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Glu Ala Leu Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu
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Ser Asn Ser Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His
125 130 135

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 35 40 45

Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
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Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
 65 70 75 80

Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
 85 90 95

Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
 100 105 110

Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
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Gln Gln Leu Gly Leu Leu Gly Cys Leu Gly His Gly Ala Leu Val Leu
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Gln Leu Leu Ser Phe Met Leu Leu Ala Gly Val Leu Val Ala Ile Leu
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cag ctg aag gct gca gtg ggt gag ttg cca gag aaa tcc aag ctg cag Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln 90 95 100 105	339
gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ttg Glu Ile Tyr Gln Glu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu 110 115 120	387
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Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala	
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acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc	261
Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala	
35 40 45	
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Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn	
50 55 60	
acc tct atg gtc acc cac ccg gac ttc gcc acg cag ccg cag cac gtt	357
Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val	
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Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln	
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Gln	Asp	His	Asp	Pro	Gly	Arg	His	Leu	Phe	Val	Gly	Gln	Leu	Ile	Gln	
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Gly	Val	Arg	Ala	Pro	Ser	Gln	His	Leu	Ser	Ser	Phe	Asp	Pro	Cys	Phe	
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Tyr	Arg	Asp	Leu	Leu	Leu	Val	His	Arg	Phe	Leu	Pro	Tyr	Glu	Met	Leu	

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345

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355 360 365

aca cag atc tac tga gtcagcatca ggggtccccag cctctgggct cctgtttcca 1276
Thr Gln Ile Tyr
370

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Met Lys Gly Trp Gly Trp Leu Ala Leu
1 5

ctt ctg ggg gcc ctg ctg gga acc gcc tgg gct cgg agg agc cag gat 219
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Lys	Glu	Tyr	Gly	Glu	Gln	Ile	Asp	Pro	Ser	Thr	His	Arg	Lys	Asn	Tyr		
90					95				100						105		
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Val	Arg	Val	Val	Gly	Arg	Asn	Gly	Glu	Ser	Ser	Glu	Leu	Asp	Leu	Gln		
				110				115						120			
ggc	atc	cga	atc	gac	tca	gat	att	agc	ggc	acc	ctc	aag	ttt	gcg	tgt		555
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			125					130					135				
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Glu	Ser	Ile	Val	Glu	Glu	Tyr	Glu	Asp	Glu	Leu	Ile	Glu	Phe	Phe	Ser		
		140					145					150					
cga	gag	gct	gac	aat	gtt	aaa	gac	aaa	ctt	tgc	agt	aag	cga	aca	gat		651
Arg	Glu	Ala	Asp	Asn	Val	Lys	Asp	Lys	Leu	Cys	Ser	Lys	Arg	Thr	Asp		
	155					160					165						
ctt	tgt	gac	cat	gcc	ctg	cac	ata	tcg	cat	gat	gag	cta	tga				693
Leu	Cys	Asp	His	Ala	Leu	His	Ile	Ser	His	Asp	Glu	Leu					
170					175					180							
accactggag	cagccacac	tggttgatg	gatcacc	cccc	aggagg	gggaa	aatggtggca										753
atgcctttta	tatattatgt	ttttactgaa	attaactgaa	aaaatatgaa	accaaagta												813
c																	814

<210> 12
 <211> 695
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (73)..(564)

<400> 12
 aagatttcag ctgcgggacg gtcaggggag acctccaggc gcaggggaagg acggccaggg 60

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tgacacggaa gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggc 111
Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
1 5 10

gcg gtg ggc gtg ggc gtc gcc gag ctc acg gaa gcc cag cgc cgg ggc 159
Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
15 20 25

ctg cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg 207
Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
30 35 40 45

gcc ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccc ttc cca 255
Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
50 55 60

gct gga ata ttt gtg agg ctg gaa ttt aag ctg cag cag aca agc tgc 303
Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
65 70 75

cgg aag agg gac tgg aag aaa ccc gag tgc aaa gtc agg ccc aat ggg 351
Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
80 85 90

agg aaa cgg aaa tgc ctg gcc tgc atc aaa ctg gcc tct gag gac aaa 399
Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
95 100 105

gtt ctg ggc cgg ttg gtc cac tgc ccc ata gag acc caa gtt ctg cgg 447
Val Leu Gly Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg
110 115 120 125

gag gct gag gag cac cag gag acc cag tgc ctc agg gtg cag cgg gct 495
Glu Ala Glu Glu His Gln Glu Thr Gln Cys Leu Arg Val Gln Arg Ala
130 135 140

ggc gag gac ccc cac agc ttc tac ttc cct gga cag ttc gcc ttc tcc 543
Gly Glu Asp Pro His Ser Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser
145 150 155

aag gcc ctg ccc cgc agc taa gccagcactg agctgcgtgg tgcctccagg 594
Lys Ala Leu Pro Arg Ser
160

accgctgccg gtggtaacca gtggaagacc ccagcccca gggagaggac cccgttctat 654

ccccagccat gataataaag ctgctctccc agctgcctct c 695

<210> 13
<211> 1451
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (105)..(1436)

<400> 13
actgcctgga aacgggctgg gcctgcctcg gacgccgccg gtgtcgcgga ttctctttcc 60

gcccgtcca tggcgggtgga tgcctgactg gaagcccagag tggg atg cgg ctg acg 116

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Met Arg Leu Thr
1

cg Arg 5	ga Lys	cg Arg	ct Leu	tg Cys	tc Ser 10	tt Phe	ct Leu	at Ile	gc Ala 15	ct Leu	ta Tyr	tg Cys	ct Leu	tt Phe	tc Ser 20	164
ct Leu	ta Tyr	gc Ala	gc Ala	ta Tyr 25	ca His	gt Val	tt Phe	tt Phe	gg Gly 30	cg Arg	cg Arg	cg Arg	ca Gln	gc Ala 35	cc Pro	212
gc Ala	gg Gly	tc Ser	cc Pro 40	cg Arg	gg Gly	ct Leu	ag Arg	aag Lys 45	gg Gly	gc Ala	gc Ala	cc Pro	gc Ala 50	cg Arg	gag Glu	260
aga Arg	cg Arg	gg Gly 55	cg Arg	gaa Glu	cag Gln	tcc Ser	act Thr 60	ttg Leu	gaa Glu	agt Ser	gaa Glu	gaa Glu 65	tgg Trp	aat Asn	cct Pro	308
tgg Trp 70	gaa Glu	gga Gly	gat Asp	gaa Glu	aaa Lys	aat Asn 75	gag Glu	caa Gln	caa Gln	cac His	aga Arg 80	ttt Phe	aaa Lys	act Thr	agc Ser	356
ctt Leu 85	caa Gln	ata Ile	tta Leu	gat Asp	aaa Lys 90	tcc Ser	acg Thr	aaa Lys	gga Gly	aaa Lys 95	aca Thr	gat Asp	ctc Leu	agt Ser	gta Val 100	404
caa Gln	atc Ile	tgg Trp	ggc Gly	aaa Lys 105	gct Ala	gcc Ala	att Ile	ggc Gly	ttg Leu 110	tat Tyr	ctc Leu	tgg Trp	gag Glu	cat His 115	att Ile	452
ttt Phe	gaa Glu	ggc Gly	tta Leu 120	ctt Leu	gat Asp	ccc Pro	agc Ser	gat Asp 125	gtg Val	act Thr	gct Ala	caa Gln	tgg Trp 130	aga Arg	gaa Glu	500
gga Gly	aag Lys	tca Ser 135	atc Ile	gta Val	gga Gly	aga Arg	aca Thr 140	cag Gln	tac Tyr	agc Ser	ttc Phe	atc Ile 145	act Thr	ggt Gly	cca Pro	548
gct Ala	gta Val 150	ata Ile	cca Pro	ggg Gly	tac Tyr	ttc Phe 155	tcc Ser	gtt Val	gat Asp	gtg Val	aat Asn 160	aat Asn	gtg Val	gta Val	ctc Leu	596
att Ile 165	tta Leu	aat Asn	gga Gly	aga Arg	gaa Glu 170	aaa Lys	gca Ala	aag Lys	atc Ile	ttt Phe 175	tat Tyr	gcc Ala	acc Thr	cag Gln	tgg Trp 180	644
tta Leu	ctt Leu	tat Tyr	gca Ala	caa Gln 185	aat Asn	tta Leu	gtg Val	caa Gln	att Ile 190	caa Gln	aaa Lys	ctc Leu	cag Gln	cat His 195	ctt Leu	692
gct Ala	gtt Val	gtt Val	ttg Leu 200	ctc Leu	gga Gly	aat Asn	gaa Glu	cat His 205	tgt Cys	gat Asp	aat Asn	gag Glu	tgg Trp 210	ata Ile	aac Asn	740
cca Pro	ttc Phe	ctc Leu 215	aaa Lys	aga Arg	aat Asn	gga Gly	ggc Gly 220	ttc Phe	gtg Val	gag Glu	ctg Leu	ctt Leu 225	ttc Phe	ata Ile	ata Ile	788
tat Tyr	gac Asp 230	agc Ser	ccc Pro	tgg Trp	att Ile	aat Asn 235	gac Asp	gtg Val	gat Asp	gtt Val	ttt Phe 240	cag Gln	tgg Trp	cct Pro	tta Leu	836

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gga gta gca aca tac agg aat ttt cct gtg gtg gag gca agt tgg tca Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser 245 250 255 260	884
atg ctg cat gat gag agg cca tat tta tgt aat ttc tta gga acg att Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile 265 270 275	932
tat gaa aat tca tcc aga cag gca cta atg aac att ttg aaa aaa gat Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp 280 285 290	980
ggg aac gat aag ctt tgt tgg gtt tca gca aga gaa cac tgg cag cct Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro 295 300 305	1028
cag gaa aca aat gaa agt ctt aag aat tac caa gat gcc ttg ctt cag Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln 310 315 320	1076
agt gat ctc aca ttg tgc ccg gtc gga gta aac aca gaa tgc tat cga Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg 325 330 335 340	1124
atc tat gag gct tgc tcc tat ggc tcc att cct gtg gtg gaa gac gtg Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val 345 350 355	1172
atg aca gct ggc aac tgt ggg aat aca tct gtg cac cac ggt gct cct Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His His Gly Ala Pro 360 365 370	1220
ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn 375 380 385	1268
tgg aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu 390 395 400	1316
caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cac Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His 405 410 415 420	1364
ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser 425 430 435	1412
ttt tta atg aat aat aaa agt taa ttatcttttt gagct Phe Leu Met Asn Asn Lys Ser 440	1451

<210> 14
 <211> 72
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 14

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Met Ser Asp Ser Lys Glu Pro Arg Val Gln Gln Leu Gly Leu Leu Gly
1 5 10 15

Cys Leu Gly His Gly Ala Leu Val Leu Gln Leu Leu Ser Phe Met Leu
20 25 30

Leu Ala Gly Val Leu Val Ala Ile Leu Val Gln Val Ser Lys Val Pro
35 40 45

Ser Ser Leu Ser Gln Glu Gln Ser Glu Gln Asp Ala Ile Tyr Gln Asn
50 55 60

Leu Thr Gln Leu Lys Ala Ala Val
65 70

<210> 15
<211> 128
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct
<400> 15

Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
1 5 10 15

Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
20 25 30

Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
35 40 45

Trp Pro Thr Pro Pro Thr Arg Pro Ala Pro Ala Pro Cys His Ala Asn
50 55 60

Thr Ser Met Val Thr His Pro Asp Phe Ala Thr Gln Pro Gln His Val
65 70 75 80

Gln Asn Phe Leu Leu Tyr Arg His Cys Arg His Phe Pro Leu Leu Gln
85 90 95

Asp Val Pro Pro Ser Lys Cys Ala Gln Pro Val Phe Leu Leu Leu Val
100 105 110

Ile Lys Ser Ser Pro Ser Asn Tyr Val Arg Arg Glu Leu Leu Arg Arg
115 120 125

<210> 16

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<211> 50
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 16

Met Lys Gly Trp Gly Trp Leu Ala Leu Leu Leu Gly Ala Leu Leu Gly
1 5 10 15

Thr Ala Trp Ala Arg Arg Ser Gln Asp Leu His Cys Gly Ala Cys Arg
20 25 30

Ala Leu Val Asp Glu Leu Glu Trp Glu Ile Ala Gln Val Asp Pro Lys
35 40 45

Lys Thr
50

<210> 17
<211> 135
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 17

Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val Gly
1 5 10 15

Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly Leu Gln Val
20 25 30

Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala Phe Gln
35 40 45

Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro Ala Gly Ile
50 55 60

Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys Arg Lys Arg
65 70 75 80

Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly Arg Lys Arg
85 90 95

Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys Val Leu Gly
100 105 110

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Arg Leu Val His Cys Pro Ile Glu Thr Gln Val Leu Arg Glu Ala Glu
115 120 125

Glu His Gln Glu Thr Gln Cys
130 135

<210> 18
<211> 148
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 18

Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr
1 5 10 15

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg
20 25 30

Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala
35 40 45

Pro Ala Arg Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu
50 55 60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg
65 70 75 80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr
85 90 95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu
100 105 110

Trp Glu His Ile Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala
115 120 125

Gln Trp Arg Glu Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe
130 135 140

Ile Thr Gly Pro
145